

Fig. 1

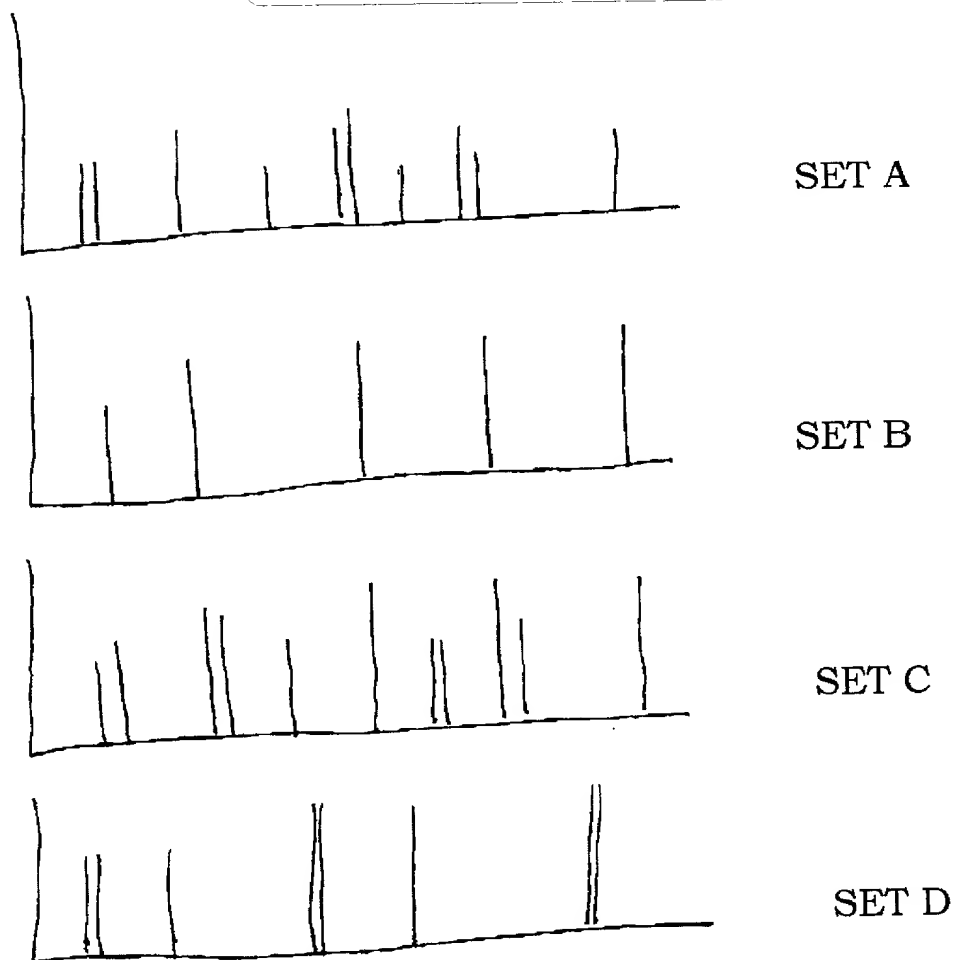
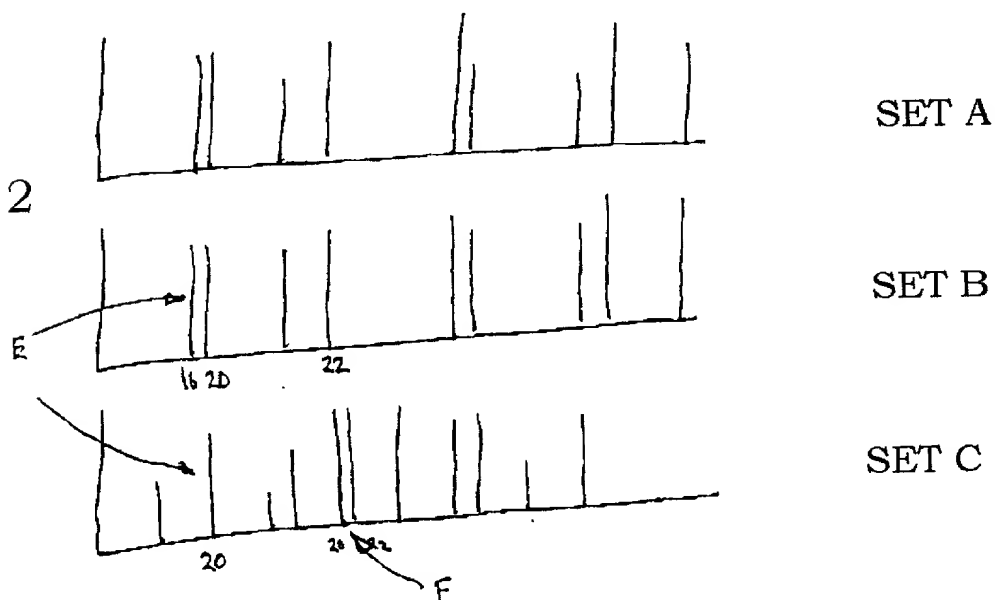


Fig. 2



T O E T 1 0 " 2 2 2 4 2 3 3 0

M_j	$P(M_j)$	$R_1(12)$	$R_2(16)$	$R_3(12,16)$	Products
12 12	f_{12}^2	$p(D)p(C)$	$p(D)p(C)f_{16}$	$p(D)p(C)f_{16}$	$p(D)^3 p(C)p(D)p(C)^2 f_{12}^2 f_{16}^2$
12 16	$2f_{12}f_{16}$	$p(D)p(C)p(D)$	$p(D)p(C)p(D)$	$p(D)^2 p(C)$	$2 p(D)^4 p(C)^2 p(D)^2 f_{12}^2 f_{16}^2$
16 16	f_{16}^2	$p(D)p(C)f_{12}$	$p(D)p(C)$	$p(D)p(C)f_{12}$	$p(D)^3 p(C)p(D)p(C)^2 f_{12}^2 f_{16}^2$
					Denominator= sum of above

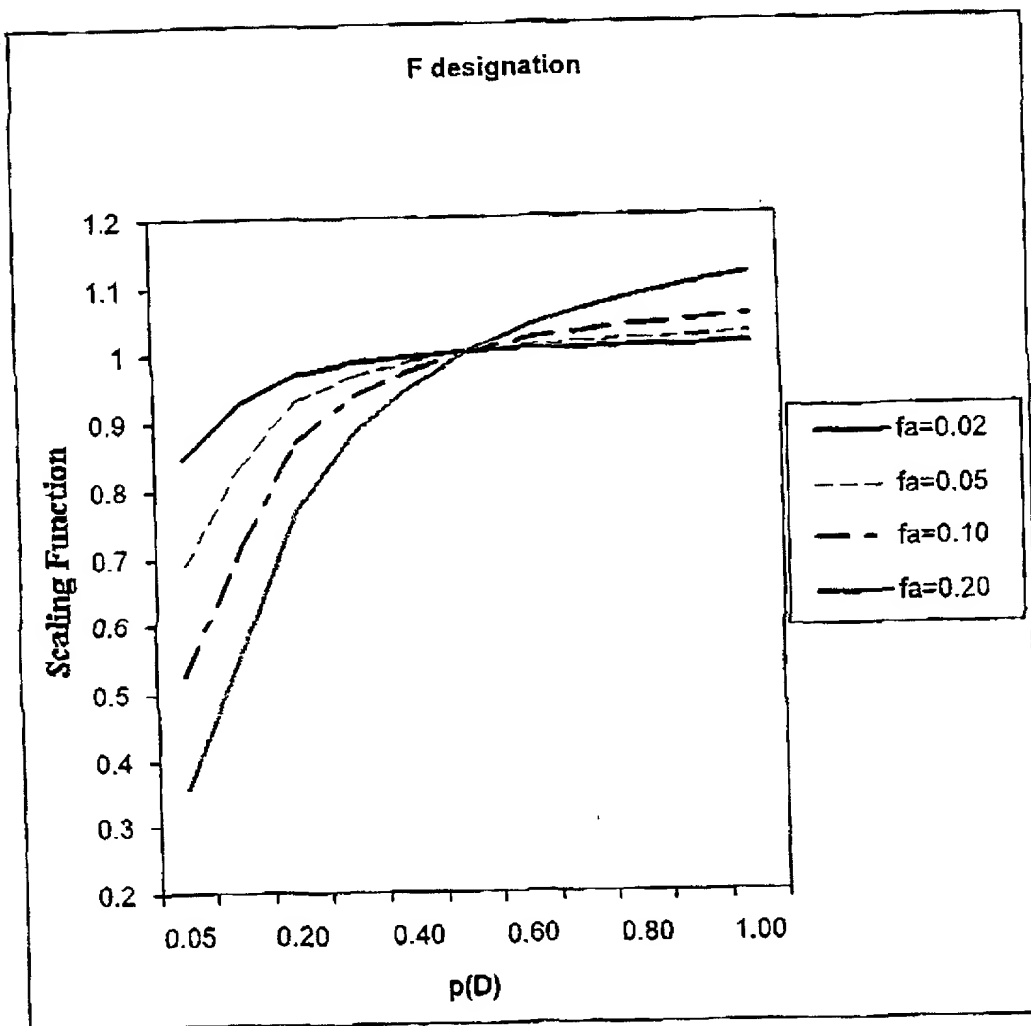
Table 1: Calculation of the components of the likelihood ratio for an example where 3 replicates show evidence of spurious bands and allele drop-out.

Fig. 3

M_j	$P(M_j)$	$R_1=abc$	$R_2=ac$	Products
ab	$2f_a f_b$	$p(D)^2 p(C) f_a p(S)^2$	$p(D)p(D)p(C)f_a p(S)^2$	$2f_a f_b f_c^2 p(D)^2 p(D)^2 p(D)p(C)^2 p(S)^4$
ac	$2f_a f_c$	$p(D)^2 p(S) (p(S)p(C) + p(S)p(C)f_a)$	$p(D)^2 p(C)p(S)^2$	$2f_a f_c p(D)^4 p(C)p(S)^3 [p(S)p(C) + p(S)p(C)f_a]$
bc	$2f_b f_c$	$p(D)^2 p(C)f_a p(S)$	$p(D)p(D)p(C)f_a p(S)^2$	$2f_b^2 f_c f_a p(D)^2 p(D)p(C)^2 p(S)^3$

Table 2: Derivation of equation 12. Note that $p(\bar{S})$ only appears once when $M_j=bc$ and $R_1=abc$ because b must be in part or wholly allelic.

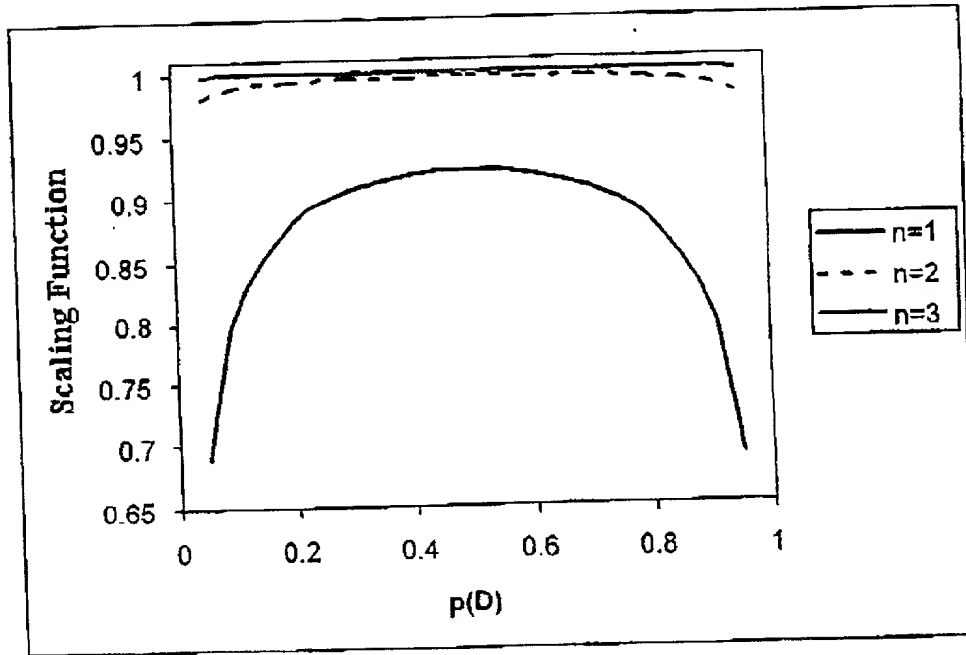
Fig. 4



Testing the robustness of the F designation: The F designation is conservative provided that the expression $\frac{1}{1 + \frac{1-2p(D)}{2p(D)} f_a} \geq 1.0$ (from equation 7).

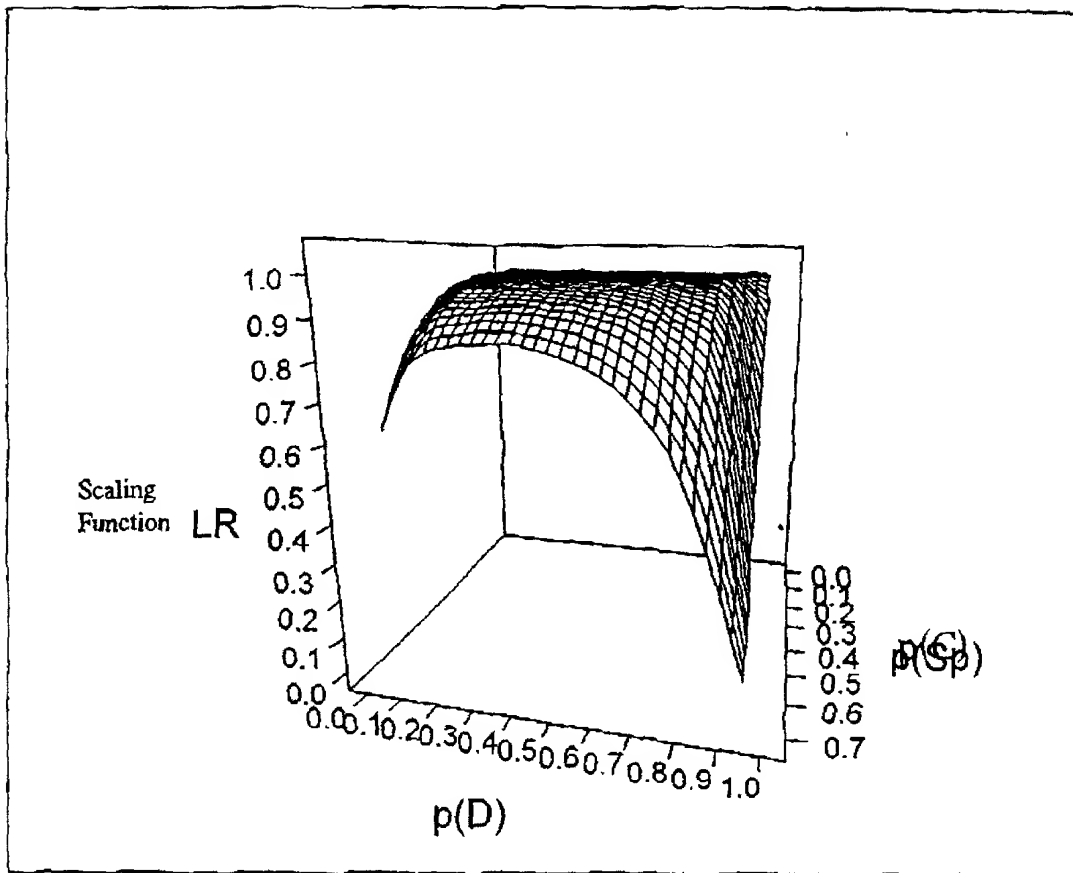
Allele frequencies (f_a) 0.02, 0.05, 0.10 and 0.20 are tested. Generally the F designation is conservative provided $p(D) > 0.5$.

Fig. 5



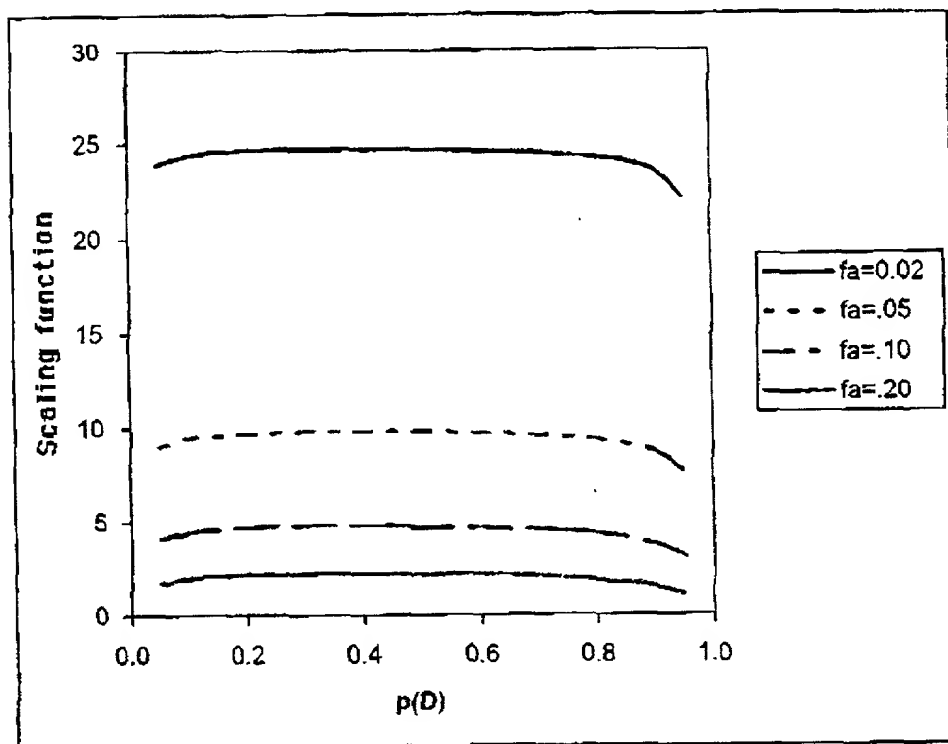
Evaluation of $\frac{1}{1 + \frac{f_a f_b^{n-1} p(C)^n}{2p(D)[p(D)p(C)]^n}}$ from equation 9 (called the scaling function). When n (the number of replicates where the genotype is ab) is greater than or equal to 2 and $R_1 = a$, then the $LR \geq 1/2f_a f_b$. When $n=1$, $1/2f_a$ would be used which is always conservative. In fig 2a $p(C)=0.3$; $f_a=f_b=0.1$.

Fig. 6a



The 3 dimensional model showing the relationships between $p(C)$ and $p(D)$ when $f_a=0.1$. The scaling function $\square 1.0$ for moderate and low values of $p(C)$ and for all intermediate values of $p(D)$.

Fig. 6b

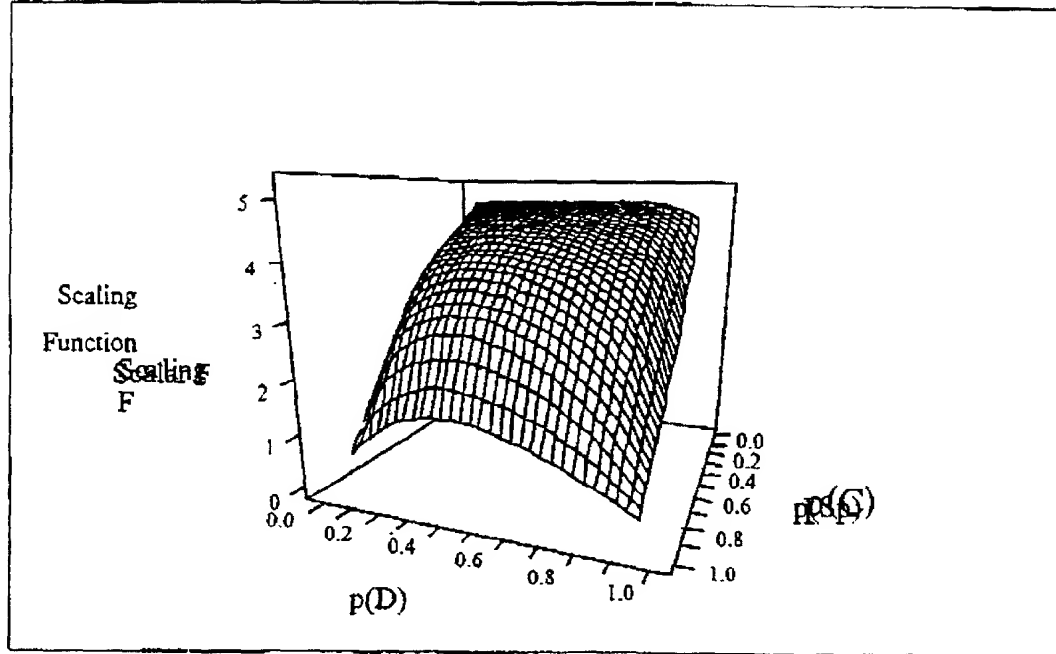


Provided that the scaling function $\frac{1}{f_a \left[2 + \frac{f_b p(D) p(C)}{p(\bar{D}) p(\bar{C})} + \frac{f_b p(C)}{2 p(\bar{D}) p(D) p(\bar{C})} \right]} \geq 1.0$

(from equation 10) then $1/2f_b$ is conservative. Allele frequencies are $f_a = f_b = 0.02, 0.05, 0.1, 0.2$ respectively and

Fig. 7a

$p(C)=0.3$.



3- dimensional graph to show the combined effect of $p(D)$ and $p(C)$ when $f_a=0.10$. The critical point where the scaling function >1 is reached when $p(C)<0.9$ and $p(D)<0.9$.

Fig. 7b

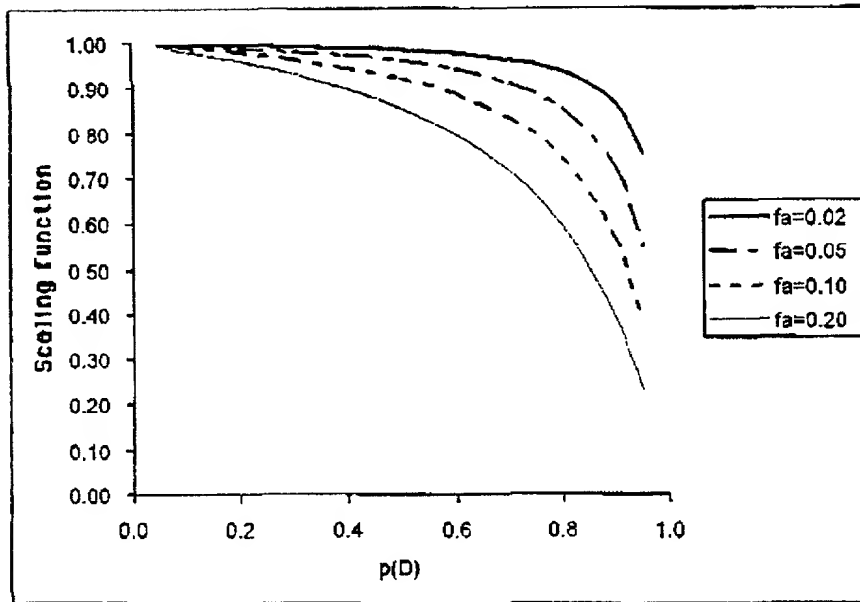
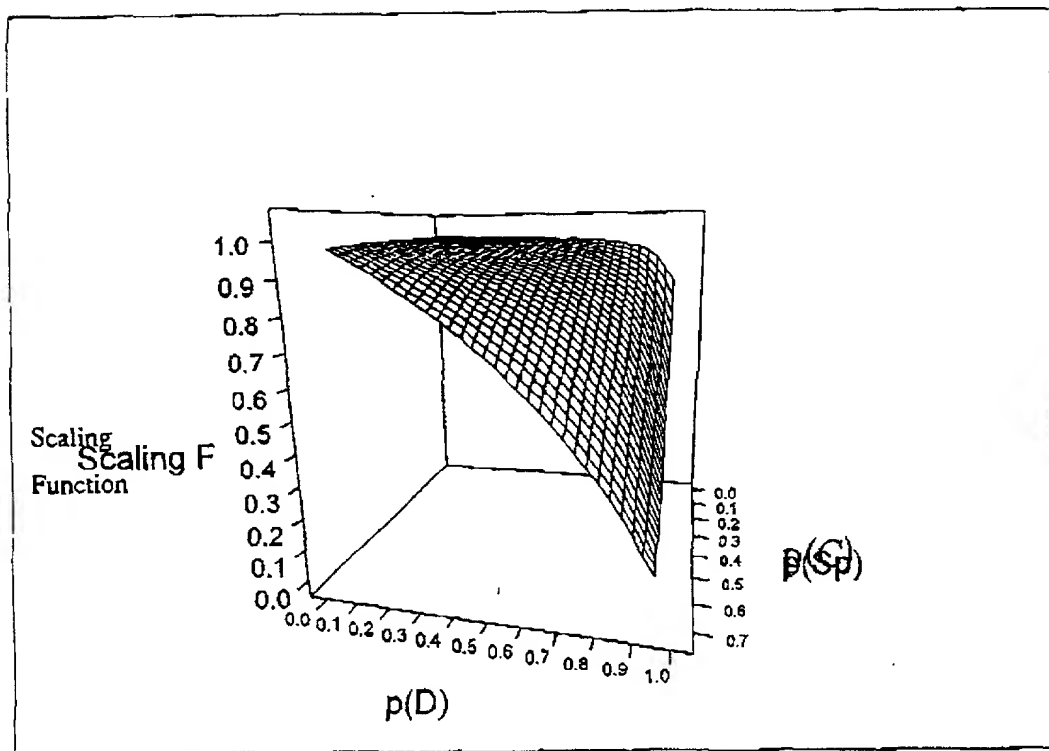
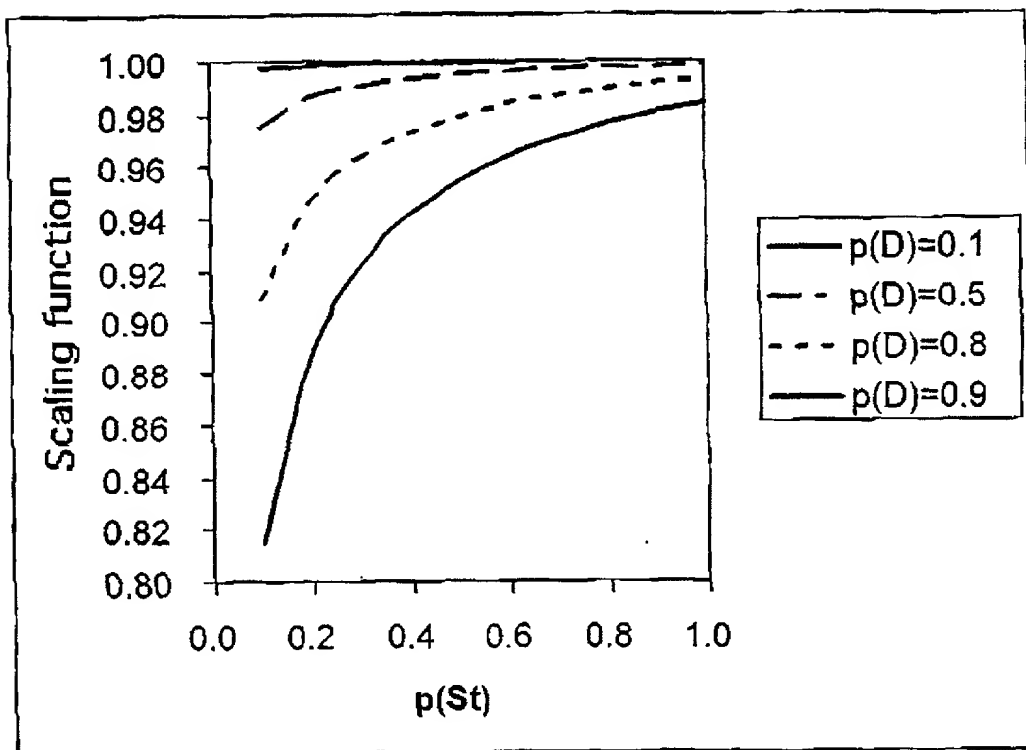


Fig. 8a



When $f_0 = 1$, the LR ≥ 1 when $p(D) < 0.5$ and $p(C) < 0.3$.

Fig. 8b



Plots of scaling function

$$1 + \frac{p(C)^2 p(D) f_a (f_a + p(\bar{St}) f_c)}{p(\bar{C}) p(\bar{D}) \{p(St) p(\bar{C}) + p(\bar{St}) p(C) f_b\}}$$

(equation 12) v. $p(St)$ for several levels of $p(D)$ ranging from 0.1 - 0.9. $p(C)=0.3$ and $f_a=f_b=f_c=0.1$.

Fig. 9

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$p(D)$	Amel	D1S432	D2S1328	D8S1179	HUM1ND1	HUMVWEA317A	D2S1328	HUMF18A (FOA)	D1S8539	D1S551	D2S1328	MAN
$p(D_{H_1})$	0.40	0.80	0.60	0.86	0.32		0.32					0.84
$p(D_{H_2})$					0.32			0.20	0.44	0.32	0.20	0.32
$p(D_{H_3})$					0.64		0.64	0.66	0.40	0.36	0.70	0.88

Table 3: Analysis of $p(D)$ parameters derived from Table 1 of Gill et al [1].

Fig. 10